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Quantitative cDNA-AFLP reveals the extent of transcriptional polymorphism in developing cotton fibres.

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Genetic variability in fibre quality among the two major cultivated cotton species, *Gossypium hirsutum* (Gh) and *G. barbadense* (Gb), shows a complex multigenic inheritance. We developed a quantitative 3 targeting cDNA-AFLP analysis strategy in order to dissect transcriptional regulation differences between the developing fibres of these 2 species. Two studies were undertaken. In the first study the expression profiles of over 3000 transcripts from the 2 parental species were analysed by quantitative cDNA-AFLP during the time-course of fibre development, between 6 and 28 days post anthesis (dpa). The 2nd study (4400 transcripts profiled) focused on two key developmental stages of fibre development (10 and 22 dpa, respectively) at a population-wide level using an inter-specific RIL population. Major achievements include: (1) the partitioning of genes among significant expression profiles and its comparison between Gh and Gb; and (2) the mapping of a large (>5000) number of expression QTLs on the RIL genetic map and a comparison of their distributions with QTL for fibre phenotypic traits. This research is part of a larger project aimed at the genetic and genomic dissection of cotton fibre quality.